



X11600.ST25.txt
SEQUENCE LISTING

<110> Becker, Gerald

Hale, John

Heath, William

Johnstone, Edward

Little, Sheila

Tu, Yuan

Yeh, Wu-Kuang

Yin, Tinggui

<120> Amyloid Precursor Protein Protease and Related Nucleic Acid
Compounds

<130> X-11600

<160> 5

<170> PatentIn version 3.1

<210> 1

<211> 1683

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (25)..(1629)

<223>

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<221> misc_feature

<222> (25)..(1629)

X11600.ST25.txt

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Met Gly Val His Val Gly Ala Ala Leu Gly Ala Leu Trp Phe Cys Leu
10               15               20               25

aca gga gcc ctg gag gtc cag gtc cct gaa gac cca gtg gtg gca ctg      147
Thr Gly Ala Leu Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu
30               35               40

gtg ggc acc gat gcc acc ctg tgc tgc tcc ttc tcc cct gag cct ggc      195
Val Gly Thr Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly
45               50               55

ttc agc ctg gca cag ctc aac ctc atc tgg cag ctg aca gat acc aaa      243
Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys
60               65               70

cag ctg gtg cac agc ttt gct gag ggc cag gac cag ggc agc gcc tat      291
Gln Leu Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr
75               80               85

gcc aac cgc acg gcc ctc ttc ccg gac ctg ctg gca cag ggc aac gca      339
Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala
90               95               100               105

tcc ctg agg ctg cag cgc gtg cgt gtg gcg gac gag ggc agc ttc acc      387
Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr
110               115               120

tgc ttc gtg agc atc cgg gat ttc ggc agc gct gcc gtc agc ctg cag      435
Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln
125               130               135

gtg gcc gct ccc tac tcg aag ccc agc atg acc ctg gag ccc aac aag      483
Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu Pro Asn Lys
140               145               150

gac ctg cgg cca ggg gac acg gtg acc atc acg tgc tcc agc tac cag      531
Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser Ser Tyr Gln
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ggc tac cct gag gct gag gtg ttc tgg cag gat ggc cag ggt gtg ccc      579
Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro
170               175               180               185

ctg act ggc aac gtg acc acg tcg cag atg gcc aac gag cag ggc ttg      627
Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu Gln Gly Leu
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Phe Asp Val His Ser Ile Leu Arg Val Val Leu Gly Ala Asn Gly Thr
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Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp	Ala	Thr															
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Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu Gln Pro Leu Lys			
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<213> Homo sapiens

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<223> The 'Xaa' at location 421 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

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<223> The 'Xaa' at location 423 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

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<222> (424)..(424)

<223> The 'Xaa' at location 424 stands for Lys, Asn, Arg, Ser, Thr, Ile

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<223> The 'Xaa' at location 426 stands for Lys, Asn, Arg, Ser, Thr, Ile
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<223> The 'Xaa' at location 427 stands for Lys, Asn, Arg, Ser, Thr, Ile
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<223> n = any nucleotide A, C, G, or T
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Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu
35      40      45
Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn

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50 55 60
 Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
 65 70 75 80
 Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe
 85 90 95
 Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val
 100 105 110
 Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp
 115 120 125
 Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys
 130 135 140
 Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr
 145 150 155 160
 Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val
 165 170 175
 Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
 180 185 190
 Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu
 195 200 205
 Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
 210 215 220
 Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln
 225 230 235 240
 Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val
 245 250 255
 Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro
 260 265 270
 Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr
 275 280 285
 Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly
 290 295 300
 Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln

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<213> Homo sapiens

<220>

<221> CDS

<222> (25)..(1629)

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<220>

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<222> (25)..(1629)

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atg	ggt	gtg	cat	gtg	ggt	gca	gcc	ctg	gga	gca	ctg	99
Met	Gly	Val	His	Val	Gly	Ala	Ala	Leu	Gly	Ala	Leu	
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aca	gga	gcc	ctg	gag	gtc	cag	gtc	cct	gaa	gac	cca	147
Thr	Gly	Ala	Leu	Glu	Val	Gln	Val	Pro	Glu	Asp	Pro	
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gtg	ggc	acc	gat	gcc	acc	ctg	tgc	tgc	tcc	tcc	cct	195
Val	Gly	Thr	Asp	Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	
			45				50					55
ttc	agc	ctg	gca	cag	ctc	aac	ctc	atc	tgg	cag	ctg	243
Phe	Ser	Leu	Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	
		60				65					70	
cag	ctg	gtg	cac	agc	ttt	gct	gag	ggc	cag	gac	cag	291
Gln	Leu	Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	
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gcc	aac	cgc	acg	gcc	ctc	ttc	ccg	gac	ctg	ctg	gca	339
Ala	Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	
90					95					100		105
tcc	ctg	agg	ctg	cag	cgc	gtg	cgt	gtg	gcg	gac	gag	387
Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	
				110					115			120
tgc	ttc	gtg	agc	atc	cgg	gat	ttc	ggc	agc	gct	gcc	435
Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	
			125					130				135
gtg	gcc	gct	ccc	tac	tcg	aag	ccc	agc	atg	acc	ctg	483
Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	

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140					145					150						
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tac Tyr	agc Ser	tgc Cys 220	ctg Leu	gtg Val	cgc Arg	aac Asn	ccc Pro 225	gtg Val	ctg Leu	cag Gln	cag Gln	gat Asp 230	gcg Ala	cac His	agc Ser	723
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acc Thr	gaa Glu	ggc Gly 300	cgg Arg	gac Asp	cag Gln	ggc Gly	agc Ser 305	gcc Ala	tat Tyr	gcc Ala	aac Asn	cgc Arg 310	acg Thr	gcc Ala	ctc Leu	963
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gtg Val	ttc Phe	tgg Trp	cag Gln	gat Asp	ggg Gly	cag Gln	ggt Gly	gtg Val	ccc Pro	ctg Leu	act Thr	ggc Gly	aac Asn	gtg Val	acc Thr	1251

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Leu Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg					
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Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu					
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Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp					
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Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn
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Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
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Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val
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Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp
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Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys
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Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr
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Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val
165 170 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
180 185 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu
195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
210 215 220

Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln
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Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val
245 250 255

Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro
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Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr
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 Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly
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 Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val
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 Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu
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 Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser
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 Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln
 385 390 395 400
 Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu
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 Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala
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gc	1682